

0280

#2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/825,580

DATE: 04/19/2001
TIME: 12:17:56

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\04192001\I825580.raw

ENTERED

3 <110> APPLICANT: Eppihimer, Michael J.
4 Schaub, Robert G.
5 Harris, Alan
7 <120> TITLE OF INVENTION: Inhibition of Thrombosis by Treatment with
8 P-Selectin Antagonists
10 <130> FILE REFERENCE: GFN-5398
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/825,580
C--> 13 <141> CURRENT FILING DATE: 2001-04-02
15 <150> PRIOR APPLICATION NUMBER: 60/193,787
16 <151> PRIOR FILING DATE: 2000-03-31
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1649
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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32 gggacacactg ggcagatgaa gcgcgagaaaag ctttgggtcc cctgcttgcg cgggaccgga 180
34 gacaggccac cgaatatgag taccttagatt atgatttctt gccagaaaacg gagcctccag 240
36 aaatgctgag gaacagact gacaccactc ctctgactgg gccttggaaacc cctgagtcta 300
38 ccactgtgga gcctgctgca aggcgttcta ctggcttggta tgcaggagggg gcagtcacag 360
40 agctgaccac ggagctggcc aacatggggaa acctgtccac ggattcaga gctatggaga 420
42 tacagaccac tcaaccagca gccacggagg cacagaccac tccacttggca gccacagagg 480
44 cacagacaac tcgactgtacg gccacggagg cacagaccac tccacttggca gccacagagg 540
46 cacagaccac tccaccagca gccacggaaag cacagaccac tcaaccacca ggccttggagg 600
48 cacagaccac tgcaccagca gccatggagg cacagaccac tgcaccagca gccatggaaag 660
50 cacagaccac tccaccagca gccatggagg cacagaccac tcaaaccaca gccatggagg 720
52 cacagaccac tgcaccagaa gccacggagg cacagaccac tcaaccacca gccacggagg 780
54 cacagaccac tccacttggca gccatggagg ccctgtccac agaaccctgt gccacagagg 840
56 ccctgtccat ggaacctact accaaaagag gtctttcat accctttct gtgtcctctg 900
58 ttactcaca gggcatcccc atggcagcca gcaatttgc cgtcaactac ccagtgggg 960
60 ccccgaccca catctctgtg aagcagtgcc tgctggccat ctaatctt ggcgtgggtgg 1020
62 ccactatctt cttegtgtgc actgtgggtgc tggcggtccg cctctcccg aaggccaca 1080
64 tgtacccctgt gcgtaattac tccccccaccc agatgtctg catctcatcc ctgttgcctg 1140
66 atgggggtga gggccctct gccacagcca atggggccct gtccaaaggcc aagagcccg 1200
68 gcctgacgcc agagccagg gaggaccgtg agggggatga ctcacccctg cacagcttcc 1260
70 tcccttagct cactctgcca tctgttttg caagacccca ctcacccctg ctctccttgg 1320
72 ccacccctga gtgcccagac cccaatccac agctctggc ttcctcggag accccctgggg 1380
74 atggggatct tcaggaaagg aactctggcc acccaaacag gacaagagca gcttggggcc 1440
76 aagcagacgg gcaagtggag ccaccttctt ctcacccctg cggatgaagc ccagccacat 1500
78 ttcaagccag gtcacaggca ggaggccatt tacttggagac agattctctc ctccctggc 1560
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85 <210> SEQ ID NO: 2
86 <211> LENGTH: 402

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87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
90 <400> SEQUENCE: 2
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94 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
95     20          25          30
97 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
98     35          40          45
100 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
101    50          55          60
103 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
104    65          70          75          80
106 Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
107     85          90          95
109 Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
110     100         105         110
112 Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
113     115         120         125
115 Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr
116     130         135         140
118 Arg Leu Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu
119    145         150         155         160
121 Ala Gln Thr Thr Pro Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro
122     165         170         175
124 Thr Gly Leu Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala Gln
125     180         185         190
127 Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Pro Pro Ala Ala
128     195         200         205
130 Met Glu Ala Gln Thr Thr Gln Thr Thr Ala Met Glu Ala Gln Thr Thr
131     210         215         220
133 Ala Pro Glu Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu
134    225         230         235         240
136 Ala Gln Thr Thr Pro Leu Ala Ala Met Glu Ala Leu Ser Thr Glu Pro
137     245         250         255
139 Ser Ala Thr Glu Ala Leu Ser Met Glu Pro Thr Thr Lys Arg Gly Leu
140     260         265         270
142 Phe Ile Pro Phe Ser Val Ser Ser Val Thr His Lys Gly Ile Pro Met
143     275         280         285
145 Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
146     290         295         300
148 Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
149    305         310         315         320
151 Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
152     325         330         335
154 Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
155     340         345         350
157 Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
158     355         360         365

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160 Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
161 370 375 380
163 Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu Thr Leu His Ser Phe
164 385 390 395 400
166 Leu Pro
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 942
172 <212> TYPE: DNA
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175 <220> FEATURE:
176 <221> NAME/KEY: CDS
177 <222> LOCATION: (1)..(939)
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182 1 5 10 15
184 agc ttg cag ctg tgg gac acc tgg gca gat gaa gcc gag aaa gcc ttg 96
185 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
186 20 25 30
188 ggt ccc ctg ctt gcc cg^g gac cgg aga cag gcc acc gaa tat gag tac 144
189 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
190 35 40 45
192 cta gat tat gat ttc ctg cca gaa acg gag cct cca gaa atg ctg agg 192
193 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
194 50 55 60
196 aac agc act gac acc act cct ctg act ggg cct gga acc cct gag tct 240
197 Asn Ser Thr Asp Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
198 65 70 75 80
200 acc act gtg gag cct gct gc^g cg^g cac aca tgc cca cc^g tgc cca 288
201 Thr Thr Val Glu Pro Ala Ala Arg Pro His Thr Cys Pro Pro Cys Pro
202 85 90 95
204 gca cct gaa gcc ctg ggg gca cc^g tca gtc ttc ctc ttc ccc cca aaa 336
205 Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
206 100 105 110
208 ccc aag gac acc ctc atg atc tcc cg^g acc cct gag gtc aca tgc gtg 384
209 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
210 115 120 125
212 gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac 432
213 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
214 130 135 140
216 gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cc^g cg^g gag gag 480
217 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
218 145 150 155 160
220 cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac 528
221 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
222 165 170 175
224 cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 576
225 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
226 180 185 190

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228	gcc	ctc	cca	gtc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	624
229	Ala	Leu	Pro	Val	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
230	195					200				205							
232	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cg	gag	gag	atg	672
233	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	
234	210					215				220							
236	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	720
237	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
238	225					230			235			240					
240	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	768
241	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
242	245					250			255								
244	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	816
245	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
246	260					265			270								
248	tat	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	864
249	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	
250	275					280			285								
252	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	912
253	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
254	290					295			300								
256	aag	agc	ctc	tcc	ctg	tcc	ccg	ggt	aaa	tga							942
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271					20				25			30					
273	Gly	Pro	Leu	Leu	Ala	Arg	Asp	Arg	Arg	Gln	Ala	Thr	Glu	Tyr	Glu	Tyr	
274					35			40			45						
276	Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu	Thr	Glu	Pro	Pro	Glu	Met	Leu	Arg	
277					50			55			60						
279	Asn	Ser	Thr	Asp	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gly	Thr	Pro	Glu	Ser	
280					65			70			75			80			
282	Thr	Thr	Val	Glu	Pro	Ala	Ala	Arg	Pro	His	Thr	Cys	Pro	Pro	Cys	Pro	
283					85			90			95						
285	Ala	Pro	Glu	Ala	Leu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
286					100			105			110						
288	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
289					115			120			125						
291	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
292					130			135			140						
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295					145			150			155			160			

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297 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
298 165 170 175
300 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
301 180 185 190
303 Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
304 195 200 205
306 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
307 210 215 220
309 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
310 225 230 235 240
312 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
313 245 250 255
315 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
316 260 265 270
318 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
319 275 280 285
321 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
322 290 295 300
324 Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 305 310

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/825,580

DATE: 04/19/2001
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Input Set : A:\seqlist.txt
Output Set: N:\CRF3\04192001\I825580.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date